

(3)

701 TTGCGCGCAAGCCGCTTTCTACACCATCAACCTCATCATCCCCGTGTG 750
||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
698 TTGTCGCAAAACCACTCTTCTACACTATCAACCTCATCATCCCCGTGTA 747
||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
751 CTCATCACCTCGCTAGCCATCCTTGTCTTCTACCTGCCATCCGACTGTGG 800
||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
748 CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG 797
||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
801 CGAGAAGATGACGTTGTGCATCTCAGTGCTGGCGCTCACGGTCTTCC 850
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
798 TGAAAAGATGACACTTGTATTTCTGTGCTGCTAGCACTCACGGTGTCC 847
||||| ||||| ||| ||| ||| ||| ||| ||| |||
851 TGCTGCTCATCTCCAAGATCGTGCCTCCCACCTCCCTCGACGTGCCGCTC 900
||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||
848 TGCTGCTCATCTCCAAGATTGTGCCTCCCACCTCCCTCGATGTACCGCTG 897
||||| ||||| ||| ||| ||| ||| ||| |||
901 GTGGCAAGTACCTCATGTTACCATGGTGCTTGTACCTTCTCCATCGT 950
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
898 GTGGGCAAGTACCTCATGTTACCATGGTGCTAGTCACCTTCTCCATCGT 947
||||| ||||| ||| ||| ||| ||| ||| |||
951 CACCAAGCGTGTGCGTGCTAACGTGCACCACCGCTCGCCACACGCACA 1000
||||| ||||| ||| ||| ||| ||| ||| ||| |||
948 CACCAAGCGTGTGCGCTAACATGTGCACCACCGCTCGCCACACGCACA 997
||||| ||||| ||| ||| ||| ||| |||
1001 CCATGGCCCTGGGTGAAGGTGCTTCTGGAGAAGCTGCCCGCGCTG 1050
||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
998 CCATGGCCCTGGGTCAAGGTGGTCTTCTGGAGAAGCTGCCACCCCTG 1047
||||| ||||| ||| ||| ||| ||| |||
1051 CTCTTCATGCAGCAGCCACGCCATCATTGCGCCCGTCAGCGCCCTGCGCCT 1100
||||| ||||| ||| ||| ||| ||| ||| |||
1048 CTCTTCCTGCAGCAGCCACGCCACCGCTGTGCACGTCAAGCGTCTGCGCTT 1097
||||| ||||| ||| ||| ||| |||
1101 GCGGCGACGCCAGCGTGAGCGCGAGGGCGCTGGAGCCCTTTCTCCGCG 1150
| ||| ||| ||| ||| ||| ||| ||| |||
1099 GAGGAGGCGCCAGCGAGAGCGTGAGGGC...GAGGCGGTTTCTCCGTG 1144
||||| ||||| ||| ||| ||| |||
1151 AAGCCCCAGGGGCCACTCCTGCACGTGCTTGTCAACCGCGCGTCGGTG 1200
||| ||| ||| ||| ||| ||| ||| |||
1145 AAGGTCCCTGCGGCTGACCCATGTACCTGCTTGTCAACCCCTGCATCAGTG 1194
||||| ||||| ||| ||| ||| |||
1201 CAGGGGTTGGCGGGGCCCTCGGGGCTGAGCCTGCACCAAGTGGCGGGCCC 1250
||||| ||| ||| ||| ||| ||| |||
1195 CAGGGCTTGGCTGGGCTTCCGAGCTGAGCCCACTGCA...GCCGGCCC 1241
||||| ||||| ||| ||| |||
1251 CGGGCGCTCAGGGGAGCCGTGTGGCTGTGGCCTCCGGGAGGCAGTGGACG 1300
||||| ||| ||| ||| ||| ||| |||
1242 GGGCGCTCTGTGGGCCATGCAGCTGTGGCCTCCGGGAAGCAGTGGATG 1291
||||| ||||| ||| ||| |||
1301 GCGTGCCTCATCGCAGACCATGCGGAGCGAGGACGATGACCAAGAGC 1350
||||| ||| ||| ||| ||| ||| |||
1292 GCGTACGCTTCATTGCGGACCATGCGAAGTGAGGATGATGACCAAGAGT 1341
||||| ||||| ||| ||| |||
1351 GTGAGTGAGGACTGGAAGTACGTGCGCATGGTGATCGACCGCCTTTCC 1400
||||| ||| ||| ||| ||| |||
1342 GTGAGGGAGGACTGAAATACGTTGCCATGGTGATCGACCGCCTGTTCC 1391

PstI

1401 CTGGATCTTGTCTTGTCTGTCTTTGGCACCATCGGCATGTTCTGC 1450
||||||||||||||||||||||||||||||||||||||||||||||||||||
1392 GTGGATCTTGTCTTGTCTGTCTGTCTTTGGGACCGTCGGCATGTTCTGC 1441
1451 AGCCTCTCTTCCAGAACTACACCACCACCTTCCACTCAGACCA 1500
||||||||||||||||||||||||||||||||||||||||
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTTCCACCCCTGACCA 1491
1501 TCAGCCCCAGCTCCAAGTGA 1521
||||||||||||||||
1492 TCAGCTCCCAGCTCCAAGTGA 1512

(4)

10/14

1 ATGCCCGCTGGCATGGCCCGGCGCTGGCGCCCGTGGCGCTGCTCCTTGG 50
1 ATGCTGGCTTGCATGGCCGGGCACTCCAACATCAATGGCGCTGTTCAAG 47
51 CTTCGGCCTCCTCCGGCTGTGCTCAGGGTGTGGGTACGGATACAGAGG 100
48 CTTCAGCCTTCTTGGCTGTGCTCAGGGTTTGGGAAC TGACACAGAGG 97
101 AGCGGCTGGTGGAGCATCTCCTGGATCCTCCGCTACAACAAGCTTATC 150
98 AGCGGCTAGTGGAGCATCTCTTAGATCCCTCCGCTATAACAAGCTGATT 147
151 CGCCCAGCCACCAATGGCTCTGAGCTGGTACAGTACAGCTTATGGTGT 200
148 CGTCCAGCTACTAACGGCTCTGAGCTGGTACTGTACAGCTCATGGTATC 197
201 ACTGGCCAGCTCATCAGTGTGCATGAGCGGGAGCAGATCATGACCACCA 250
198 ATTGGCTCAGCTCATTAGTGTGCACGAGCGGGAGCAGATCATGACCACCA 247
251 ATGTCTGGCTGACCCAGGAGTGGGAAGATTATGCCCTCACCTGGAAGCCT 300
248 ATGTCTGGCTGACCCAGGAGTGGGAAGATTACCGCCTCACATGGAAGCCT 297
301 GAAGAGTTGACAACATGAAGAAAGTTGGCTCCCTCCAAACACATCTG 350
298 GAGGACTTCGACAATATGAAGAAAGTCCGGCTCCCTCCAAACACATCTG 347

FIG. 9a-1

SUBSTITUTE SHEET

11/14

351 GCTCCCAGATGTGGTCTGTACAACAATGCTGACGGCATGTACGAGGTGT 400
348 GCTCCCAGATGTGGTCTATACAACAATGCTGACGGCATGTACGAAGTCT 397
401 CCTTCTATTCCAATGCCGTGGTCTCCTATGATGGCAGCATTCTGGCTG 450
398 CCTTCTATTCCAATGCTGTGGTCTCCTATGATGGCAGCATTGGCTA 447
· SphI ·
451 CCGCCTGCCATCTACAAGAGGTGCATGCAAGATTGAAGTAAAGCACTTCCC 500
448 CCACCTGCCATCTACAAGAGGTGCATGCAAGATTGAGGTGAAGCACTTCCC 497
501 ATTTGACCAGCAGAACTGCACCATGAAGTTCCGTTGTGGACCTACGACC 550
498 ATTTGACCAGCAGAAATTGCACCATGAAGTTCGCTATGGACCTACGACC 547
551 GCACAGAGATCGACTTGGTCTGAAGAGTGAGGTGGCCAGCCTGGACGAC 600
548 GTACTGAGATTGACCTGGTCTCAAAAGTATGTGGCCAGTCTGGATGAC 597
601 TTCACACCTAGTGGTGAGTGGGACATCGTGGCGCTGCCGGCCGCGCAA 650
598 TTCACACCCAGCAGGGAGTGGGACATCATCGCACTGCCAGGCCGACGCAA 647
651 CGAGAACCCCGACGACTCTACGTACGTGGACATCACGTATGACTTCATCA 700
648 CGAGAACCCAGACGACTCCACCTATGTGGACATCACCTATGACTTCATCA 697

FIG.9a-2

SUBSTITUTE SHEET

12/14

701 TTCGCCGCAAGCCGCTTTCTACACCATCAACCTCATCCCCTGTGTG 750
698 TTCGTCGCAAACCACTTTCTACACTATCAACCTCATCCCCTGCGTA 747
751 CTCATCACCTCGCTAGCCATCCTGTCTTCTACCTGCCATCCGACTGTGG 800
748 CTCATCACCTCGCTGGCCATCCTGGTCTTCTACCTGCCCTCAGACTGTGG 797
801 CGAGAAGATGACGTTGTGCATCTCAGTGCTGGCGCTCACGGTCTTCC 850
798 TGAAAAGATGACACTTGTATTCCTGTGCTGCTAGCACTCACGGTGTTC 847
851 TGCTGCTCATCTCCAAGATCGTGCCTCCCACCTCCCTCGACGTGCCGCTC 900
848 TGCTGCTCATCTCCAAGATTGTGCCTCCCACCTCCCTCGATGTACCGCTG 897
901 GTCGGCAAGTACCTCATGTTACCATGGTGCCTGTCACCTTCTCCATCGT 950
898 GTGGGCAAGTACCTCATGTTACCATGGTGCAGTCACCTTCTCCATCGT 947
951 CACCAGCGTGTGCGTGCTAACGTGCACCACCGCTGCCACCACGCACA 1000
948 CACCAGCGTGTGCTCAATGTGCACCACCGCTGCCCTACCACGCACA 997
1001 CCATGGGCCCTGGGTGAAGGTGCTTCCCTGGAGAAGCTGCCCGCGCTG 1050
998 CCATGGCCCCCTGGGTCAAGGTGGTCTTCCCTGGAGAAGCTGCCACCCTG 1047

FIG. 9b-1

13/14

1051 CTCTTCATGCAGCAGCCACGCCATCATTGCGCCCGTCAGCGCCCTGCGCCT 1100
1048 CTCTTCCTGCAGCAGCCACGCCACCGCTGTGCACGTCAAGCGTCTGCGCTT 1097
1101 GCGGCGACGCCAGCGTGAGCGCGAGGGCGCTGGAGCCCTCTTCTTCCCGCG 1150
1098 GAGGAGGCGCCAGCGAGAGCGTGAGGGC...GAGGGGTTTCTTCCGTG 1144
1151 AAGCCCCAGGGGCCGACTCCTGCACGTGCTTCGTCAACCGCGCGTCGGTG 1200
1145 AAGGTCCCTGCGGCTGACCCATGTACCTGCTTGTCAACCCCTGCATCAGTG 1194
1201 CAGGGGTTGGCCGGGGCCTTCGGGGCTGAGCCTGCACCAAGTGGCGGGCCC 1250
1195 CAGGGCTTGGCTGGGCTTCCGAGCTGAGCCCAGTGCA...GCCGGCCC 1241
1251 CGGGCGCTCAGGGGAGCCGTGTGGCTGTGGCCTCCGGAGGGCGGTGGACG 1300
1242 GGGGCGCTCTGTGGGGCCATGCAGCTGTGGCCTCCGGAAAGCAGTGGATG 1291
1301 GCGTGCCTTCATCGCAGACCACATGCGGAGCGAGGACGATGACCAGAGC 1350
1292 GCGTACGCTTCATTGCGGACCACATGCGAAGTGAGGATGATGACCAGAGT 1341
1351 GTGAGTGAGGACTGGAAGTACGTGCCATGGTATCGACCCCTCTTCCT 1400
1342 GTGAGGGAGGACTGGAATACTGTTGCCATGGTATCGACCCCTGTTCCCT 1391

FIG.9b-2

14/14

1401 CTGGATCTTGTCTTGTCTGTCTTTGGCACCATCGGCATGTTCTGC 1450
1392 GTGGATCTTGTCTTGTCTGTCTTTGGGACCGTCGGCATGTTCTGC 1441
1451 AGCCTCTCTTCCAGAACTACACCAACCAACCTCCTCCACTCAGACCAAC 1500
1442 AGCCTCTCTTCCAGAACTACACTGCCACTACCTCCTCCACCCCTGACCAAC 1491
1501 TCAGCCCCCAGCTCCAAGTGA 1521
1492 TCAGCTCCCAGCTCCAAGTGA 1512

FIG.9c